PatentIn.prjSubstitute.ST25.txt
SEQUENCE LISTING

#10

<110>   Cyclacel

<120>   Compositions and Methods for Monitoring the Modification of Modification
Dependent Binding Partner Polypeptides

<130>   10069/1062

<140>   09/770102

<141>   2001-01-25

<150>   US 60/179283

<151>   2000-01-31

<160>   57

<170>   PatentIn version 3.1

<210>   1

<211>   17

<212>   PRT

<213>   Unknown

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<222>   (1)..(17)

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<400>   1

Met Leu Cys Cys Met Arg Arg Thr Lys Gln Val Glu Lys Asn Asp Asp
1   5   10   15

Asp

<210> 2

<211> 10

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<213> Unknown

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<400> 2

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1   5   10

<210> 3

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<213> Unknown

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<222> (1)..(30)

<223> ubiquitination site

<400> 3

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1               5               10              15

Arg Asp Gly Leu Lys Lys Glu Arg Leu Leu Asp Asp Arg His
            20              25              30
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<210> 4

<211> 21

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<222> (1)..(21)

<223> ubiquitination site

<400> 4

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1               5               10              15

Thr Thr Leu Ala Pro
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<210> 5

<211> 10

<212> PRT

<213> Unknown

<220>

<223> O-GlcNAc site

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<221> DOMAIN

<222> (1)..(10)

<223> O-GlcNAc site

<400> 5

Gly Thr Thr Ser Thr Ile Gln Thr Ala Pro
1   5   10

<210> 6

<211> 12

<212> PRT

<213> Unknown

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<223> O-GlcNAc site

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<222> (1)..(12)

<223> O-GlcNAc site

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Ser Ala Val Ser Ser Ala Asp Gly Thr Val Leu Lys
1   5   10

<210> 7

<211> 18

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<213> Unknown

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<222> (1)..(18)

<223> O-GlcNAc site

<400> 7

Asp Ser Ser Thr Asp Leu Thr Gln Thr Ser Ser Ser Gly Thr Val Thr
1   5   10   15

Leu Pro

<210> 8

<211> 12

<212> PRT

<213> Unknown

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<222> (1)..(12)

<223> O-GlcNAc site

<400> 8

Met Ala Gly Gly Pro Ala Asp Thr Ser Asp Pro Leu
1   5   10

<210> 9

<211> 13

<212> PRT

<213> Unknown

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<223> O-GlcNAc site

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<222> (1)..(13)

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<400> 9

Ala Gln Thr Ile Thr Ser Glu Thr Pro Ser Ser Thr Thr
1   5   10

<210> 10

<211> 8

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<222> (1)..(8)

<223> Xaa at position 6 may be any amino acid

<220>

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<222> (1)..(8)

<223> Xaa at position 3 may be any amino acid

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Arg Arg Xaa Arg Arg Xaa Ser Thr
1   5

<210> 11

<211> 5

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<213> Unknown

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<222> (1)..(5)

<223> Consensus sequence, each Xaa is any amino acid

<220>

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<222> (1)..(5)

<223> X at posistion 2, 3, and 5 can be any amino acid

<400> 11

Lys Xaa Xaa Ser Xaa
1   5

<210> 12

<211> 3

<212> PRT

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<222> (1)..(3)

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<222> (1)..(3)

<223> X at posistion 2 can be any amino acid

<400> 12

Arg Xaa Thr
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<210> 13

<211> 5

<212> PRT

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<223> Consensus sequence, each Xaa is any amino acid

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Arg Xaa Xaa Ser Xaa
1   5

<210> 14

<211> 4

<212> PRT

<213> Unknown

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<222> (1)..(4)

<223> Consensus sequence, each Xaa is any amino acid

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<222> (1)..(4)

<223> X at posistion 1 and 4 can be any amino acid

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Xaa Ser Arg Xaa
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<210> 15

<211> 8

<212> PRT

<213> Unknown

<220>

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<223> Consensus sequence, each Xaa is any amino acid

<220>

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<222> (1)..(8)

<223> X at posistion 1, 3, 4, 6 and 8 can be any amino acid

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Xaa Arg Xaa Xaa Ser Xaa Arg Xaa
1   5

<210> 16

<211> 6

<212>   PRT

<213>   Unknown

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<222>   (1)..(6)

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<222>   (1)..(6)

<223>   X at posistion 1, 3, 4, and 6 can be any amino acid

<400>   16

Xaa Arg Xaa Xaa Ser Xaa
1   5

<210>   17

<211>   6

<212>   PRT

<213>   Unknown

<220>

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<221>   DOMAIN

<222>   (1)..(6)

<223>   Consensus sequence

<400>   17

Ser Glu Leu Ser Arg Arg

1   5

<210> 18

<211> 6

<212> PRT

<213> Unknown

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<223> Consensus sequence, each Xaa is any amino acid

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<222> (1)..(6)

<223> X at posistion 1,3,4, and 6 can be any amino acid

<400> 18

Xaa Ser Xaa Xaa Ser Xaa
1   5

<210> 19

<211> 5

<212> PRT

<213> Unknown

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<223> Consensus sequence, each Xaa is any amino acid

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<222> (1)..(5)

<223> X at posistion 1, 3, and 5 can be any amino acid

<400> 19

Xaa Ser Xaa Glu Xaa
1   5

<210> 20

<211> 7

<212> PRT

<213> Unknown

<220>

<223> Consensus sequence

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<221> DOMAIN

<222> (1)..(7)

<223> Consensus sequence, each Xaa is any amino acid

<220>

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<222> (1)..(7)

<223> X at poaiation a, 3, 4, 5, and 7 can be any amino acid

<400> 20

Xaa Ser Xaa Xaa Xaa Ser Xaa
1   5

<210> 21

<211> 9

<212> PRT

<213> Unknown

<220>

<223> Consensus sequence

<220>

<221> DOMAIN

<222> (1)..(9)

<223> Consensus sequence

<400> 21

Gly Ser Ser Lys Ser Lys Pro Lys Asp
1   5

<210> 22

<211> 9

<212> PRT

<213> Unknown

<220>

<223> Consensus sequence

<220>

<221> DOMAIN

<222> (1)..(9)

<223> Consensus sequence

<400> 22

Gly Cys Ile Lys Ser Lys Arg Lys Asp
1   5

<210> 23

<211> 9

<212> PRT

<213>   Unknown

<220>

<223>   Consensus sequence

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<221>   DOMAIN

<222>   (1)..(9)

<223>   Consensus sequence

<400>   23

Gly Cys Ile Lys Ser Lys Glu Asp Lys
1   5

<210>   24

<211>   9

<212>   PRT

<213>   Unknown

<220>

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<222>   (1)..(9)

<223>   Consensus sequence

<400>   24

Gly Cys Val Gln Cys Lys Asp Lys Glu
1   5

<210>   25

<211>   9

<212>   PRT

<213>   Unknown

<220>

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<222> (1)..(9)

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Gly Cys Thr Leu Ser Ala Glu Asp Lys
1   5

<210> 26

<211> 9

<212> PRT

<213> Unknown

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Gly Cys Ile Lys Ser Lys Arg Lys Asp
1   5

<210> 27

<211> 9

<212> PRT

<213> Unknown

<220>

<223> Consensus sequence

<220>

<221> DOMAIN

<222> (1)..(9)

<223> Consensus sequence

<400> 27

Gly Cys Val Gln Cys Lys Asp Lys Glu
1   5

<210> 28

<211> 9

<212> PRT

<213> Unknown

<220>

<223> Consensus sequence

<220>

<221> DOMAIN

<222> (1)..(9)

<223> Consensus sequence

<400> 28

Gly Cys Thr Leu Ser Ala Glu Asp Lys
1   5

<210> 29

<211> 4

<212> PRT

<213> Unknown

<220>

<223> Consensus sequence

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<221> DOMAIN

<222> (1)..(4)

<223> Consensus sequence, Xaa is any amino acid

<220>

<221> MISC_FEATURE

<222> (1)..(4)

<223> X at posistion 2 can be any amino acid

<400> 29

Asn Xaa Ser Thr
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<210> 30

<211> 4

<212> PRT

<213> Unknown

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<223> C-terminal sequence

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<222> (1)..(4)

<223> C-terminal sequence

<400> 30

His Ser Thr Val
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<210> 31

<211> 92

<212> DNA

<213> Artificial Sequence

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<222> (1)..(92)

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gggggggagct ctgggaggcg gaggtggagg gctgatgcgc cagctgcagg atgaagttga   60

agaactggaa caggaaaact ggcatctgca ga   92

<210> 32

<211> 96

<212> DNA

<213> Artificial Sequence

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<220>

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<222> (1)..(96)

<223> Synthetic primer

<400> 32
ccccccctcga gttattaaac ttcggcttcc aggcactgaa cttcacgcag cagacgggca   60

acttcgttct gcagatgcca gttttcctgt tccagt   96

<210> 33

<211> 37

<212> PRT

<213> Unknown

<220>

<223> Coiled-coil sequence

<220>

<221> DOMAIN

<222> (1)..(37)

<223> Coiled coil sequence

<400> 33

Leu Met Arg Gln Leu Gln Asp Glu Val Glu Glu Leu Glu Gln Glu Asn
1   5   10   15

Trp His Leu Gln Asn Glu Val Ala Arg Leu Leu Arg Glu Val Gln Cys
                20   25   30

Leu Glu Ala Glu Val
                35

<210> 34

<211> 37

<212> PRT

<213> Unknown

<220>

<223> Coiled coil sequence

<220>

<221> DOMAIN

<222> (1)..(37)

<223> Coiled coil sequence

<400> 34

Arg Met Arg Gln Leu Glu.Asp Arg Val Glu Glu Leu Arg Glu Gln Asn
1   5   10   15

Trp His Leu Ala Asn Gln Val Ala Arg Leu Arg Gln Arg Val Cys Glu
                20,   25   30

Leu Lys Ala Arg Val
                35

<210> 35

<211> 80

<212> DNA

<213> Artificial Sequence

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<221> misc_feature

<222> (1)..(80)

<223> Synthetic primer

<400> 35

gtaccgctag ctcttacaag ggtattgctc agttggagca ggaaatcgcc caattagaac   60

aagaaaatgc acaacttgaa   80

<210> 36

<211> 73

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<220>

<221> misc_feature

<222> (1)..(61)

<223> Synthetic primer

<400> 36

gggcatcgat ttcctgctca agctgagcga tctcttgttc aagttgtgca ttttcttgtt   60

ctaattgggc gat   73

<210> 37

<211> 31

<212> PRT

<213> Unknown

<220>

<223> Sequence for cloning

<220>

<221> DOMAIN

<222> (1)..(31)

<223> Sequence for cloning

<400> 37

Tyr Lys Gly Ile Ala Gln Leu Glu Gln Glu Ile Ala Gln Leu Glu Gln
1   5   10   15

Glu Asn Ala Gln Leu Glu Gln Glu Ile Ala Gln Leu Glu Gln Glu
            20   25   30

<210> 38

<211> 38

<212> PRT

<213> Unknown

<220>

<223> Coiled coil sequence

<220>

<221> DOMAIN

<222> (1)..(38)

<223> Coiled coil sequence

<400> 38

Tyr Lys Gly Ile Cys Gln Leu Arg Gln Arg Ile Ala Gln Leu Arg Gln
1   5   10   15

Arg Asn Ala Gln Leu Arg Gln Arg Ile Ala Gln Leu Arg Gln Arg Ile
                20   25   30

Ala Gln Leu Arg Gln Arg
            35

<210> 39

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<220>

<221> PEPTIDE

<222> (1)..(36)

<223> Synthetic peptide

<400> 39

Arg Cys Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly
1   5   10   15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
                20   25   30

Asp Val Leu Asp
            35

<210> 40

<211> 36

<212> PRT

<213> Artificial Sequence

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<223> Synthetic peptide

<220>

<221> PEPTIDE

<222>   (1)..(36)

<223>   Synthetic peptide

<400>   40

Arg Cys Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly
1   5   10   15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            20   25   30

Asp Val Leu Asp
        35

<210>   41

<211>   33

<212>   DNA

<213>   Artificial Sequence

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<223>   Synthetic primer

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<221>   misc_feature

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ggaattcggg cactgctgtt ggggcaggcc tcc   33

<210> 43

<211> 23

<212> DNA

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<223> Synthetic primer

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<221> misc_feature

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<400> 43
gggggcccag agtgaagttc agc   23

<210> 44

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Synthetic primer

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<221> misc_feature

<222> (1)..(23)

<223> Synthetic primer

<400> 44
gggggcccga gcccccccgcg tac   23

<210> 45

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Synthetic primer

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<221> misc_feature

<222> (1)..(23)

<223> Synthetic primer

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gggggcccaa ccagctctat aac   23

<210> 46

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Synthetic primer

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<221> misc_feature

<222> (1)..(23)

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ggggatccgc gaggggggcag ggc   23

<210> 47

<211> 36

<212> PRT

<213> Artificial Sequence

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<223> Synthetic peptide

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<221> PEPTIDE

<222> (1)..(36)

<223> Synthetic peptide

<400> 47

Arg Cys Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly
1   5   10   15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
                20   25   30

Asp Val Leu Asp
            35

<210> 48

<211> 6

<212> PRT

<213> Unknown

<220>

<223> Cleavage site

<220>

<221> MISC_FEATURE

<222> (1)..(6)

<223> X at posistion 6 can be any amino acid

<220>

<221> SITE

<222> (1)..(6)

<223> Clavage site, X can be any mino acid

<400> 48

Trp Leu Glu His Asp Xaa
1   5

<210> 49

<211> 5

<212> PRT

<213> Unknown

<220>

<223> Cleavage site

<220>

<221> SITE

<222> (1)..(5)

<223> Cleavage site, each Xaa is any amino acid

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> X at posistion 3 and 5 can be any amino acid

<400> 49

Asp Glu Xaa Asp Xaa
1   5

<210> 50

<211> 6

<212> PRT

<213> Unknown

<220>

<223> Cleavage site

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<222> (1)..(6)

<223> Cleavage site, Xaa is any amino acid

<220>

<221> MISC_FEATURE

<222> (1)..(6)

<223> X at posistion 4 and 6 can be any amino acid

<400> 50

Leu Val Glu Xaa Asp Xaa
1   5

<210> 51

<211> 5

<212> PRT

<213> Unknown

<220>

<223> Cleavage site

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<222> (1)..(5)

<223> Cleavage site, Xaa is any amino acid

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> X at posistion 5 can be any amino acid

<400> 51

Ile Glu Gly Arg Xaa
1   5

<210> 52

<211> 8

<212> PRT

<213> Unknown

<220>

<223> Cleavage site

<220>

<221> SITE

<222> (1)..(8)

<223> Cleavage site, each Xaa is any amino acid

<220>

<221> MISC_FEATURE

<222> (1)..(8)

<223> X at posistion 3 and 5 can be any amino acid

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Glu Asn Xaa Tyr Xaa Gln Ser Gly
1   5

<210> 53

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Tag peptide

<220>

<221> PEPTIDE

<222> (1)..(5)

<223> Tag peptide

<400> 53

Arg Tyr Ile Arg Ser
1   5

<210> 54

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Tag peptide

<220>

<221> PEPTIDE

<222> (1)..(6)

<223> Tag peptide

<400> 54

Asp Thr Tyr Arg Tyr Ile
1   5

<210> 55

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Tag peptide

<220>

<221> PEPTIDE

<222> (1)..(6)

<223> Tag peptide

<400> 55

Thr Asp Phe Leu Tyr Lys
1   5

<210> 56

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Tag peptide

<220>

<221> PEPTIDE

<222> (1)..(9)

<223> Tag sequence

<400> 56

Glu Glu Glu Glu Tyr Met Pro Met Glu
1   5

<210> 57

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Tag peptide

<220>

<221> PEPTIDE

<222> (1)..(11)

<223> Tag sequence

<400> 57

Lys Pro Pro Thr Pro Pro Pro Glu Pro Glu Thr
1   5   10